RAW SEQUENCE LISTING   DATE: 07/19/2001
PATENT APPLICATION: US/09/899,513   TIME: 15:22:09

Input Set : **A:\LEX-0200-USA SEQLIST.txt**
Output Set: **N:\CRF3\07192001\I899513.raw**

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 4 <110> APPLICANT: Hu, Yi
 5        Turner, C. Alexander Jr.
 6        Nepomnichy, Boris
 7        Scoville, John
 8        Walke, D. Wade
10 <120> TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding
the Same
12 <130> FILE REFERENCE: LEX-0200-USA
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/899,513
C--> 14 <141> CURRENT FILING DATE: 2000-07-05
14 <150> PRIOR APPLICATION NUMBER: US 60/217,600
15 <151> PRIOR FILING DATE: 2000-07-11
17 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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22 <211> LENGTH: 618
23 <212> TYPE: DNA
24 <213> ORGANISM: homo sapiens
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29 gctcgcttca tcgtggtgcc cgcggcctat gccttggcac tgggcctggg gctgccagcc   180
30 aacgtggcgg ccctggcaat gttcatccgc agcggcgggc gcctgggcca ggccctgctt   240
31 ctctacctgt tcaacctggc tctggttgat gagttcttca cgctcacgct gcagctgtgg   300
32 ctcacctact acctgggcct ggcccggagg ccgcctgcca cgcggccggg gccacctact   360
33 acgtgtccac ctatgcggcg gtggtcttcg ccgcgctcat cagcgtgtgc cgctgcggct   420
34 tcgtacgcgg tcccgggccc agggcggctg cccgcctggc ccggtgccta cggbgccccg   480
35 cgcgcgctgc ctgcgccttc gcctggctgg cgggcctggc ccctccctgc ctggagcacc   540
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37 tgctcgcggc caacgtga                                                 618
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40 <211> LENGTH: 205
41 <212> TYPE: PRT
42 <213> ORGANISM: homo sapiens
44 <400> SEQUENCE: 2
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48              20                  25                  30
49 Gly Cys Ser Leu Trp Asp Asp Pro Ala Arg Phe Ile Val Val Pro Ala
50          35                  40                  45
51 Ala Tyr Ala Leu Ala Leu Gly Leu Gly Leu Pro Ala Asn Val Ala Ala
52      50                  55                  60
53 Leu Ala Met Phe Ile Arg Ser Gly Gly Arg Leu Gly Gln Ala Leu Leu
54 65                  70                  75                  80
55 Leu Tyr Leu Phe Asn Leu Ala Leu Val Asp Glu Phe Phe Thr Leu Thr
56                  85                  90                  95
57 Leu Gln Leu Trp Leu Thr Tyr Tyr Leu Gly Leu Ala Arg Arg Pro Pro
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59 Ala Thr Arg Pro Gly Pro Pro Thr Thr Cys Pro Pro Met Arg Arg Trp
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61 Ser Ser Pro Arg Ser Ser Ala Cys Ala Ala Ala Ala Ser Tyr Ala Val
62     130                 135                  140
63 Pro Gly Pro Gly Arg Leu Pro Ala Trp Pro Gly Ala Tyr Gly Ala Pro
64 145                 150                  155                  160
65 Arg Ala Leu Pro Ala Pro Ser Pro Gly Trp Arg Ala Trp Pro Leu Pro
66                 165                 170                  175
67 Ala Trp Ser Thr Ala Gly Gln Ala Arg Gly Trp Pro Pro Pro Arg Trp
68             180                 185                  190
69 Pro Ser Arg Pro Pro Ser Cys Trp Cys Ser Arg Pro Thr
70          195                 200                  205
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74 <212> TYPE: DNA
75 <213> ORGANISM: homo sapiens
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79  ctacgtgggt ttactgcaca ggtctgtggc ccaacatgta tgaaccatac tccatctgtg   120
80  aggggcatct ctaccctctc agtcactaag gttggaaatt tccaagttat ctaggactcc   180
81  tgcctcttcc tcgcttccca cagtttgtca ccaaaaactc tggagtccat accctcctct   240
82  cagcagctgc tggccaggtt cggtcttcat tccctctcac atggactctg cctctagtgt   300
83  cccctcccag caagggctga agaagaggag actggggtgg gagaaggtgg aatggggget   360
84  gcctttgtcg ctagcctccg cagtaacctt tcttctgcca cttcaaggtc agagatgaac   420
85  agcagtgttg gggacctggg tgttggcggc tgcagcctct gggatgaccc tgctcgcttc   480
86  atcgtggtgc ccgcggccta tgccttggca ctgggcctgg ggctgccagc caacgtggcg   540
87  gccctggcaa tgttcatccg cagcggcggg cgcctgggcc aggccctgct tctctacctg   600
88  ttcaacctgg ctctggttga tgagttcttc acgctcacgc tgcagctgtg gctcacctac   660
89  tacctgggcc tggcccggag gccgcctgcc acgcggccgg ggccacctac tacgtgtcca   720
90  cctatgcggc ggtggtcttc gccgcgctca tcagcgtgtg ccgctgcggc ttcgtacgcg   780
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92  cctgcgcctt cgcctggctg gcgggcctgg cccctccctg cctggagcac cgctgggcaa   900
93  gctcgggget ggcctccgcc acggtggcct tcgcggccgc cttcctgctg gtgctcgcgg   960
94  ccaacgtgag cctggcgcgg gcgctcaagg cgccctctgg cccgggcccg ggccctgcaa  1020
95  ccgccggcgc gcaccggcgc gcggccaaga ccatggtcct ggggttcctg ctggtcttcg  1080
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102 ctgacgcaac cacatactac ccctgtagct gtgaacctcc cagtcacctt cttaggcccg  1500
103 ggaaaatgcc ggtctcctac tcttcatggc ctttgtacct gacttggcca ggaatgatct  1560
104 ctgttcctct ctttcactaa gttagttctt cttcaccctc acttcctcta aagtaactcc  1620
105 ttatagggaa gcctttcttg gctggcaaca cacacacaca cacacacaca cacatacaca  1680
106 cacgagtgaa tcagatcgga ktgctctttg atagctcttt tcataattgt aatcaagcaa  1740
107 ttaattgggt aatgcggtgg tggtgttttc tttctctctt gccagaatgt attcatgttg  1800
108 acccataaga cattatcatt tttataagcc cccaaaagtt gaatattgga aattttattt  1860
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109 ccacccaatt caacttaata aattctgtgt ttaccttgcw maaaaaaaaa aaaaaaaaaa      1920
110 aaatcactgc tgtatctcct gtggttggca ctgcgccttg catataataa gagctcagtg      1980
111 tatcagatgc gtgagtgaaa actgaatatc attaatttaa attgcttaag tactcactca      2040
112 cacattccaa gtctgtgata gcttttccct caagtgtgtg tgagattctc caagcttg        2098
114 <210> SEQ ID NO: 4
115 <211> LENGTH: 3774
116 <212> TYPE: DNA
117 <213> ORGANISM: homo sapiens
119 <400> SEQUENCE: 4
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121 gaagaacagc caaaactgag aaaggaagca gttggatcta ttgagatatt ccgctttgct       120
122 gatggactgg acatcacact catgatcctg ggtatactgg catcactggt caatggagcc       180
123 tgccttcctt taatgccact ggttttagga gaaatgagtg ataaccttat tagtggatgt       240
124 ctagtccaaa ctaacacatc aaattatcag aactgtactc agtctcaaga gaagctgaat       300
125 gaagatatga ctctgttgcc cctgtattat gttggaatag gtgttgctgc cttgattttt       360
126 ggttacatac agatttcctt gtggattata actgcagcac gacagaccaa gaggattcga       420
127 aaacagtttt ttcattcagt tttggcacag gacatcggct ggtttgatag ctgtgacatc       480
128 ggtgaactta acactcgcat gacagatgac attgacaaaa tcagtgatgg tattggagat       540
129 aagattgctc tgttgtttca aaacatgtct actttttcga ttggcctggc agttggtttg       600
130 gttaagggct ggaaactcac cctagtgact ctatccacgt ctcctcttat aatggcttca       660
131 gcggcagcat gttctaggat ggtcatctca ttgcccagta aggaattaag tgcctattcc       720
132 aaagctgggg ctgtggcaga agaagtcttg tcatcaatcc gaacagtcat agcctttagg       780
133 gcccaggaga aagaacttca aaggtataca cagaatctca aagatgcaaa ggattttggc       840
134 ataaaaagga ctatagcttc aaaagtgtct cttggtgctg tgtacttctt tatgaatgga       900
135 acctatggac ttgcttttg gtatggaacc tccttgattc ttaatggaga acctggatat       960
136 accatcggga ctgttcttgc tgttttcttt agtgtaatcc atagcagtta ttgcattgga      1020
137 gcagcagtcc ctcactttga aaccttcgca atagcccgag gagctgcctt tcatattttc      1080
138 caggttattg ataagaaacc cagtatagat aactttttcca cagctggata taaacctgaa      1140
139 tccatagaag gaactgtgga atttaaaaat gtttctttca attatccatc aagaccatct      1200
140 atcaagattc tgaaaggtct gaatctcaga attaagtctg gagagacagt cgccttggtc      1260
141 ggtctcaatg ccagtggaaa gagtacggta gtccagcttc tgcagaggtt atatgatccg      1320
142 gatgatggct ttatcatggt ggatgagaat gacatcagag ctttaaatgt gcggcattat      1380
143 cgagaccata ttggagtggt tagtcaagag cctgtttttgt tcgggaccac catcagtaac      1440
144 aatatcaagt atggacraga tgatgtgact gatgaagaga tggagagagc agcaagggaa      1500
145 gcaaatgcgt atgatttttat catggagttt cctaataaat ttaatacatt ggtaggggaa      1560
146 aaaggagctc aaatgagtgg agggcagaaa cagaggatcg caattgctcg tgccttagtt      1620
147 cgaaacccca agattctgat tttagatgag gctacgtctg ccctggattc agaaagcrag      1680
148 tcagctgttc aagctgcact ggagaaggcg agcaaaggtc ggactacaat cgtggtagca      1740
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151 atgtcacagg atattaaaaa agctgatgaa cagatggagt caatgacata ttctactgaa      1920
152 agaaagacca actcacttcc tctgcactct gtgaagagca tcaagtcaga cttcattgac      1980
153 aaggctgagg aatccacca atctaaagag ataagtcttc ctgaagtctc tctattaaaa      2040
154 attttaaagt aaacaagcc tgaatggcct tttgtggttc tggggacatt ggcttctgtt      2100
155 ctaaatggaa ctgttcatcc agtattttcc atcatctttg caaaaattat aaccatgttt      2160
156 ggaaataatg ataaaaccac attaaagcat gatgcagaaa tttattccat gatattcgtc      2220
157 attttgggtg ttatttgctt tgtcagttat ttcatgcagg gattatttta cggcagagca      2280
158 ggggaaattt taccgatgag attaagacac ttggccttca aagccatgtt atatcaggat      2340
159 attgcctggt ttgatgaaaa ggaaaacagc acaggaggct tgacaacaat attagccata      2400
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RAW SEQUENCE LISTING   DATE: 07/19/2001
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Input Set : A:\LEX-0200-USA SEQLIST.txt
Output Set: N:\CRF3\07192001\I899513.raw

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160 gatatagcac aaaattcaagg agcaacaggt tccaggattg gcgtcttaac acaaaatgca   2460
161 actaacatgg gactttcagt tatcatttcc tttatatatg gatgggagat gacattcctg   2520
162 attctgagta ttgctccagt acttgccgtg acaggaatga ttgaaaccgc agcaatgact   2580
163 ggatttgcca acaaagataa gcaagaactt aagcatgctg gaaagatagc aactgaagct   2640
164 ttggagaata tacgtactat agtgtcatta acaagggaaa aagccttcga gcaaatgtat   2700
165 gaagagatgc ttcagactca acacagaaat acctcgaaga aagcacagat tattggaagc   2760
166 tgttatgcat tcagccatgc ctttatatat tttgcctatg cagcagggtt tcgatttgga   2820
167 gcctatttaa ttcaagctgg acgaatgacc ccagagggca tgttcatagt ttttactgca   2880
168 attgcatatg gagctatggc catcggaaaa acgctcgttt tggctcctga atattccaaa   2940
169 gccaaatcgg gggctgcgca tctgtttgcc ttgttggaaa agaaaccaaa tatagacagc   3000
170 cgcagtcaag aagggaaaaa gccagacaca tgtgaaggga atttagagtt tcgagaagtc   3060
171 tctttcttct atccatgtcg cccagatgtt ttcatcctcc gtggcttatc cctcagtatt   3120
172 gagcgaggaa agacagtagc atttgtgggg agcagcggct gtgggaaaag cacttctgtt   3180
173 caacttctgc agagacttta tgaccccgtg caaggacaag tgctgtttga tggtgtggat   3240
174 gcaaaagaat tgaatgtaca gtggctccgt tcccaaatag caatcgttcc tcaagagcct   3300
175 gtgctcttca actgcagcat tgctgagaac atcgcctatg gtgacaacag ccgtgtggtg   3360
176 ccattagatg agatcaaaga agccgcaaat gcagcaaata tccattcttt tattgaaggt   3420
177 ctccctgaga aatacaacac acaagttgga ctgaaaggag cacagctttc tggcggccag   3480
178 aaacaaagac tagctattgc aagggctctt ctccaaaaac ccaaaatttt attgktggat   3540
179 gaggccactt cagccctcga taatgacagt gagaaggtgg ttcagcatgc ccttgataaa   3600
180 gccaggacgg gaaggacatg cctagtggtc actcacaggc tctctgcaat tcagaacgca   3660
181 gatttgatag tggttctgca caatggaaag ataaaggaac aaggaactca tcaagagctc   3720
182 ctgagaaatc gagacatata ttttaagtta gtgaatgcac agtcagtgca gtga          3774
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184 <210> SEQ ID NO: 5
185 <211> LENGTH: 1257
186 <212> TYPE: PRT
187 <213> ORGANISM: homo sapiens
189 <220> FEATURE:
190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: (1)...(1257)
192 <223> OTHER INFORMATION: Xaa = Any Amino Acid
194 <400> SEQUENCE: 5

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198             20                  25                  30
199 Ser Ile Glu Ile Phe Arg Phe Ala Asp Gly Leu Asp Ile Thr Leu Met
200         35                  40                  45
201 Ile Leu Gly Ile Leu Ala Ser Leu Val Asn Gly Ala Cys Leu Pro Leu
202     50                  55                  60
203 Met Pro Leu Val Leu Gly Glu Met Ser Asp Asn Leu Ile Ser Gly Cys
204 65                  70                  75                  80
205 Leu Val Gln Thr Asn Thr Ser Asn Tyr Gln Asn Cys Thr Gln Ser Gln
206                 85                  90                  95
207 Glu Lys Leu Asn Glu Asp Met Thr Leu Leu Pro Leu Tyr Tyr Val Gly
208             100                 105                 110
209 Ile Gly Val Ala Ala Leu Ile Phe Gly Tyr Ile Gln Ile Ser Leu Trp
210         115                 120                 125
211 Ile Ile Thr Ala Ala Arg Gln Thr Lys Arg Ile Arg Lys Gln Phe Phe
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213 His Ser Val Leu Ala Gln Asp Ile Gly Trp Phe Asp Ser Cys Asp Ile
214 145                    150                    155                    160
215 Gly Glu Leu Asn Thr Arg Met Thr Asp Asp Ile Asp Lys Ile Ser Asp
216                    165                    170                    175
217 Gly Ile Gly Asp Lys Ile Ala Leu Leu Phe Gln Asn Met Ser Thr Phe
218                    180                    185                    190
219 Ser Ile Gly Leu Ala Val Gly Leu Val Lys Gly Trp Lys Leu Thr Leu
220            195                    200                    205
221 Val Thr Leu Ser Thr Ser Pro Leu Ile Met Ala Ser Ala Ala Ala Cys
222        210                    215                    220
223 Ser Arg Met Val Ile Ser Leu Pro Ser Lys Glu Leu Ser Ala Tyr Ser
224 225                    230                    235                    240
225 Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ser Ser Ile Arg Thr Val
226                    245                    250                    255
227 Ile Ala Phe Arg Ala Gln Glu Lys Glu Leu Gln Arg Tyr Thr Gln Asn
228                    260                    265                    270
229 Leu Lys Asp Ala Lys Asp Phe Gly Ile Lys Arg Thr Ile Ala Ser Lys
230            275                    280                    285
231 Val Ser Leu Gly Ala Val Tyr Phe Phe Met Asn Gly Thr Tyr Gly Leu
232        290                    295                    300
233 Ala Phe Trp Tyr Gly Thr Ser Leu Ile Leu Asn Gly Glu Pro Gly Tyr
234 305                    310                    315                    320
235 Thr Ile Gly Thr Val Leu Ala Val Phe Phe Ser Val Ile His Ser Ser
236                    325                    330                    335
237 Tyr Cys Ile Gly Ala Ala Val Pro His Phe Glu Thr Phe Ala Ile Ala
238            340                    345                    350
239 Arg Gly Ala Ala Phe His Ile Phe Gln Val Ile Asp Lys Lys Pro Ser
240            355                    360                    365
241 Ile Asp Asn Phe Ser Thr Ala Gly Tyr Lys Pro Glu Ser Ile Glu Gly
242        370                    375                    380
243 Thr Val Glu Phe Lys Asn Val Ser Phe Asn Tyr Pro Ser Arg Pro Ser
244 385                    390                    395                    400
245 Ile Lys Ile Leu Lys Gly Leu Asn Leu Arg Ile Lys Ser Gly Glu Thr
246                    405                    410                    415
247 Val Ala Leu Val Gly Leu Asn Ala Ser Gly Lys Ser Thr Val Val Gln
248            420                    425                    430
249 Leu Leu Gln Arg Leu Tyr Asp Pro Asp Asp Gly Phe Ile Met Val Asp
250            435                    440                    445
251 Glu Asn Asp Ile Arg Ala Leu Asn Val Arg His Tyr Arg Asp His Ile
252        450                    455                    460
253 Gly Val Val Ser Gln Glu Pro Val Leu Phe Gly Thr Thr Ile Ser Asn
254 465                    470                    475                    480
255 Asn Ile Lys Tyr Gly Xaa Asp Asp Val Thr Asp Glu Glu Met Glu Arg
256            485                        490                    495
257 Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu Phe Pro Asn
258            500                    505                    510
259 Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met Ser Gly Gly
260            515                    520                    525
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W--> 255 (marker)

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY　　　　　　　　DATE: 07/19/2001
PATENT APPLICATION:　US/09/899,513　　TIME: 15:22:10

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Output Set: N:\CRF3\07192001\I899513.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7